

## EXHIBIT D

ClustalW (v1.4) multiple sequence alignment

5 Sequences Aligned                      Alignment Score = 707  
Gaps Inserted = 20                      Conserved Identities = 0

Pairwise Alignment Mode: Slow  
Pairwise Alignment Parameters:  
    Open Gap Penalty = 5.0      Extend Gap Penalty = 0.1  
    Similarity Matrix: blosum

Multiple Alignment Parameters:  
    Open Gap Penalty = 5.0      Extend Gap Penalty = 0.0  
    Delay Divergent = 40%      Gap Distance = 8  
    Similarity Matrix: blosum

Processing time: 0.6 seconds

```
SEQ ID NO:5   1           MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRT 37
AA283751-1   1 FGTREN-----LPSHHEASSPFQPALYP-ASLLLHLLHRREEASC----- 39
AA283751-2   1     SERGKICLLTMRLVLSSLLCILLLCFSIFSTEGKRRPANSI----- 42
AA283751-3   1       E-----SRPFIQRR---VML---S---RT----RELRSQ----- 21
AA283751-4   1  GWSL-----LGSLVDHS---ARY---VMCAQ-GSGAKATSP----- 29
```

```
SEQ ID NO:5  38 RLCCHRVSPNSTNLKGHHVRLCKPCKLEPEPRLWVVP GALPQV 81
AA283751-1  40 -----QQPGQAGEPGSAATESLAP-TQQT 62
AA283751-2  43 -----VRQENQALLPPSP 55
AA283751-3  22 -----IR-SRQKEM 29
AA283751-4  30 -----IG-CTYCELALS---WVASF---RM 47
```